

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 10:09:32 : Search time 12.87 seconds
112,457 Million cell updates/sec

Title: US-09-486-094-12

Perfect score: 51

Sequence: 1 XXXXXXXXXXCMXC 19

Scoring Table: BLOSSUM62

Gapop 10.0 : Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR-66

1: p122

2: p122

3: p122

4: p122

Pred. No. is the number of results predicted by chance to have a score as good as or equal to the score of the result being printed.
And is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	29	56.9	117	2	JG2210		hypothetical 12.6
2	28	54.9	57	2	S59073		metallothionein 1
3	28	54.9	57	2	S59073		metallothionein 1
4	28	54.9	243	2	T37608		hypothetical prote
5	28	54.9	462	2	T00708		violaxanthin de-ep
6	28	54.9	248	2	T32664		violaxanthin de-ep
7	28	54.9	248	2	T32664		violaxanthin de-ep
8	27	52.9	58	1	SKMDS1		metallothionein 1
9	27	52.9	555	2	T77330		hypothetical prote
10	27	52.9	555	2	T77330		hypothetical prote
11	27	52.9	454	1	S23392		alpha-2-macroglob
12	27	52.9	454	1	A31102		alpha-2-macroglob
13	26	51.0	57	1	SKMDS2		metallothionein 2
14	26	51.0	57	1	SKMDS2		metallothionein 2
15	26	51.0	58	2	A70399		metallothionein 1
16	26	51.0	222	2	H83470		metallothionein 1
17	26	51.0	222	2	H83470		metallothionein 1
18	26	51.0	248	2	R71602		chitinase (EC 3.2
19	26	51.0	389	2	T16046		probable integrat
20	26	51.0	435	2	S86093		hypothetical prote
21	26	51.0	455	1	CD0901		tumor necrosis fac
22	26	51.0	455	1	CD0901		tumor necrosis fac
23	26	51.0	646	2	T33039		hypothetical prote
24	26	51.0	721	2	T41942		hypothetical prote
25	26	51.0	721	2	T41942		hypothetical prote
26	26	51.0	1002	2	T19236		hypothetical prote
27	26	51.0	1046	2	A26838		prestalk protein p
28	26	51.0	1046	2	A26838		prestalk protein p
29	26	51.0	1145	2	S71136		structural polypro

30 26 51.0 1253 1 VHWV
31 26 51.0 1253 1 VHWV
32 26 51.0 2139 2 A35971
33 26 51.0 4753 1 A47137
34 26 49.0 71 1 S2N2M
35 26 49.0 71 1 S2N2M
36 26 49.0 71 1 S47577
37 26 49.0 71 1 S39420
38 26 49.0 71 1 S39420
39 26 49.0 71 1 S39421
40 26 49.0 71 1 S39418
41 26 49.0 71 1 S39418
42 26 49.0 78 2 S48038
43 26 49.0 116 2 H72207
44 26 49.0 116 2 H72207
45 26 49.0 132 1 KNSHHC

ALIGNMENTS

RESULT 1
JC2210
Hypothetical 12.6k protein, J1M6 - trumpet lily (fragment)
C-Accession: JC2210
C-Date: 16-Jul-1999
C-Revision: 16-Jul-1999
C-Text-Change: 21-Jul-2000
DNA Res 1: 15-36 (99%)
A: Title: Characterization of cDNAs induced in meiotic prophase in lily microsporocyte
A: Accession number: P02106
A: Accession number: P02106
A: Status: preliminary
A: Molecule type: mRNA
A: Cross-references: DBJ: D21842; NID: 9431165; PDB: 9431165
Query Match 56.9% Score 29; DB 2; Length 117;
Best Local Similarity 23.5% Pred. No. 15;
Matches 4; Conservative 13; Indels 0; Gaps 0;

QY 2 CXXXXXCMXCXMC 18
DB 74 CTTSCKGVCSMKC 90
RESULT 2
S59073
metallothionein isoform 12a - blue crab
C-Accession: S59073
C-Date: 19-Mar-1997
C-Revision: 19-Mar-1997
C-Text-Change: 07-May-1999
Biochem J 311: 617-622, 1995
A: Title: Primary structure and tissue-specific expression of blue crab (Callinectes s
A: Accession: S59073
A: Accession: S59073
A: Molecule type: protein
A: Molecule type: protein
A: Keywords: metal binding
Query Match 54.9% Score 28; DB 2; Length 57;
Best Local Similarity 23.5% Pred. No. 45;
Matches 4; Conservative 13; Indels 0; Gaps 0;

QY 2 CXXXXXCMXCXMC 18
DB 33 CSSECKGVCSMKC 49
RESULT 3
S59073
metallothionein isoform 12a - blue crab
C-Accession: S59073
C-Date: 19-Mar-1997
C-Revision: 19-Mar-1997
C-Text-Change: 07-May-1999
Biochem J 311: 617-622, 1995
A: Title: Primary structure and tissue-specific expression of blue crab (Callinectes s
A: Accession: S59073
A: Accession: S59073
A: Molecule type: protein
A: Molecule type: protein
A: Keywords: metal binding
Query Match 54.9% Score 28; DB 2; Length 57;
Best Local Similarity 23.5% Pred. No. 45;
Matches 4; Conservative 13; Indels 0; Gaps 0;

Query Match 54.9%, Score 28, DB 2, Length 2448;
Best local Similarity 54.9%, Pred No. 1, 2e+02;
Matches 4, Conservative 0, Mismatches 13, Indels 0, Gaps 0;

Oy 2 CXXXXXXKXXXXXXC 18

Db 733 CTGCTGNSGSCFISC 749

RESULT 8

SMK018

hirsutiens 1 - mud crab

C-Species: Scylla serrata (mud crab)

C-Date: 29-Jul-1991 sequence_revision 29-Jul-1991 ttext_change 13-Sep-1996

P-Accession: A03283 0, Olafson, R.W.

J. Biol. Chem. 257, 2420-2426: 1982

A-Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2.

A-Accession: A03283 A03285 A03287 A03289

A-Molecule type: protein

A-Genetics: none: 3

A-Note: the five Cys-X-Cys sequences are believed to be the principal metal-binding sites

C-Superfamily: metallothionein

C-keywords: metal binding

Query Match 52.9%, Score 27, DB 1, Length 58;

Best local Similarity 52.9%, Pred No. 1, 2e+02;

Matches 4, Conservative 0, Mismatches 13, Indels 0, Gaps 0;

Oy 33 CXXXXXXKXXXXXXC 18

Db 33 CXXXXXXKXXXXXXC 49

RESULT 9

T47330

Metallothionein protein c79p10 Arabidopsis thaliana

C-Species: Arabidopsis thaliana

C-Date: 20-Apr-2000 sequence_revision 20-Apr-2000 ttext_change 20-Apr-2000

P-Accession: T47330 0, R. Flores, M. Arizono, A. De Simone, V. J. Messer, R.M., Rudd, S.

submitted to the Protein Sequence Database, April 2000

A-Reference number: 22461

A-Status: preliminary

A-Molecule type: DNA

A-Residues: 1-565 <YMLJ3663

A-Genetics: none: 3

A-Experimental source: CULTURE

A-Accession: 169/2: 232/1: 276/2: 368/3: 444/3

A-Note: F7P3.10

Query Match 52.9%, Score 27, DB 2, Length 565;

Best local Similarity 23.5%, Pred No. 1, 2e+02;

Matches 4, Conservative 0, Mismatches 13, Indels 0, Gaps 0;

Oy 2 CXXXXXXKXXXXXXC 18

Db 191 GSWVANSVWVATITC 207

RESULT 10

T20764

hypothetical protein flit1.6 - Caenorhabditis elegans

C-Species: Caenorhabditis elegans

C-Date: 15-Oct-1999 sequence_revision 15-Oct-1999 ttext_change 18-Feb-2000

C-Accession: T20764

Riheimer, S.
submitted to the EMBL Data Library, September 1995
A-Reference number: 219321
A-Status: preliminary; translated from GE/EMBL/DBJ
A-Molecule type: DNA
A-Genetics: none: 3
A-Cross-references: EMBL:T24770; PDB:CA91028.1; GSWP:GN00028; CSDP:FLICL.6
A-Experimental source: clone FLIC1
A-Accession: CSDP:FLIC1.6
A-Mes position: X
A-Accession: 30/3: 30/3: 97/1: 140/2: 190/1: 286/1: 377/3: 417/2: 499/2
A-Accession: 30/3: 30/3: 97/1: 140/2: 190/1: 286/1: 377/3: 417/2: 499/2
A-Accession: 30/3: 30/3: 97/1: 140/2: 190/1: 286/1: 377/3: 417/2: 499/2

Query Match 52.9%, Score 27, DB 2, Length 572;

Best local Similarity 23.5%, Pred No. 1, 2e+02;

Matches 4, Conservative 0, Mismatches 13, Indels 0, Gaps 0;

Oy 2 CXXXXXXKXXXXXXC 18

Db 54 CSMENCHVORCKRC 70

RESULT 11

Alpha-2-macroglobulin receptor precursor - chicken

A-Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein rece

C-Species: Gallus gallus (chicken)

C-Date: 04-Sep-1998 sequence_revision 04-Sep-1998 ttext_change 22-Jun-1999

C-Accession: A53102

R-Name: J. Stipan, S. J. Blom, P.T., Schneider, W.J.

A-Title: The somatic cell-specific low density lipoprotein receptor-related protein o

A-Reference number: A53102; MIM:94103212

A-Accession: A53102

A-Mes position: X

A-Accession: 1-453 -84M-74904; MIM:9410306; PDB:CA52870.1; PDB:438007

A-Residues: 1-453 -84M-74904; MIM:9410306; PDB:CA52870.1; PDB:438007

A-Molecule type: mRNA

A-Genetics: none: 3

A-Experimental source: CULTURE

A-Accession: 1-453 -84M-74904; MIM:9410306; PDB:CA52870.1; PDB:438007

A-Note: The alpha-2-macroglobulin receptor complex consists of noncovalently-asso

C-keywords: beta-hydroxyaspartic acid; calcium binding; glyco

P-1-17/Domain: signal sequence status predicted <SIC>

P-18-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-19-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-20-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-21-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-22-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-23-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-24-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-25-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-26-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-27-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-28-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-29-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-30-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-31-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-32-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-33-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-34-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-35-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-36-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-37-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-38-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-39-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-40-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-41-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

P-42-3942/Domain: LDL receptor WPD-containing repeat homology <N03>

F:20-294/Domain: alpha-2-macroglobulin receptor FSK chain status predicted <SK>
 F:31-315/Domain: EGF homology <EGF>
 F:73-109/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:116-148/Domain: EGF homology <EGF>
 F:190-340/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:241-28/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:241-28/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:326-377/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:380-421/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:422-459/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:572-61/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:615-66/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:615-66/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:712-75/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:734-80/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:808-84/Domain: EGF homology <EGF>
 F:896-93/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:937-97/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:1061-1088/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:1061-1088/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:1146-1189/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:1186-1222/Domain: EGF homology <EGF>
 F:1228-1262/Domain: EGF homology <EGF>
 F:1310-1356/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1357-1399/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1407-1489/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1500-1532/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1538-1577/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1584-1627/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1628-1670/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1671-1717/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1755-1794/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1798-1847/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1935-1977/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:1978-2020/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2065-2106/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2107-2155/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2160-2195/Domain: EGF homology <EGF>
 F:2245-2285/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2284-2345/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2345-2389/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2391-2474/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:2483-2518/Domain: EGF homology <EGF>
 F:2523-2562/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2563-2589/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2633-2689/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2819-2855/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:2945-2981/Domain: EGF homology <EGF>
 F:3000-3069/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3070-3114/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3133-3157/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3202-3242/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3243-3285/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3295-3321/Domain: EGF homology <EGF>

F:3325-3370/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3742-3777/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:3829-3861/Domain: EGF homology <EGF>
 F:3869-3912/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:3913-3945/Domain: alpha-2-macroglobulin receptor FSK chain status predicted <SK>
 F:3945-4421/Domain: EGF homology <EGF>
 F:4034-4037/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:4058-4100/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:4101-4143/Domain: LDL receptor WPD-containing repeat homology <WPD>
 F:4201-4232/Domain: EGF homology <EGF>
 F:4237-4268/Domain: EGF homology <EGF>
 F:4309-4340/Domain: EGF homology <EGF>
 F:4345-4375/Domain: EGF homology <EGF>
 F:4432-4445/Domain: transmembrane status predicted <TM>
 F:4445-4545/Domain: intracellular status predicted <INT>
 F:4572-4593/Modified site: erythro-beta-hydroxyaspartate (Asn) status predicted <AS>
 F:4593-4614/Modified site: aspartate (Asp) status predicted <AS>
 F:4076-4126-4179/Binding site: carbohydrate (Nan) (covenant) status predicted <NAN>

Query Match 52.94; Score 27; DB 1; Length 4545;
 Query Local Similarity 23.54; Pred. No. 1,Re+02;
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 2 CXXXXXXKXXXXX 18
 DB 2981 CAGLGGSTTFTEQGLQ 2397

RESULT 14
 SMD23
 C:Species: Scylla serrata (mud crab)
 C:Accession: A01284
 A:Residues: 1-57 <LER>
 A:Keywords: metal binding
 A:Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2.
 A:Reference number: A92363; MIMD:R214240
 A:Accession: A01284
 C:Superfamily: metallothionein
 C:Keywords: metal binding

Query Match 51.94; Score 26; DB 1; Length 57;
 Query Local Similarity 23.54; Pred. No. 1,Re+02;
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 2 CXXXXXXKXXXXX 18
 DB 33 CSSGCKNNKEDRNTC 49

RESULT 15
 A37039
 metallothionein 1 - American lobster

C:Species: Homarus americanus (American lobster)
 C>Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 12-Apr-1995
 C:Accession: A37039
 R:Browser: M. P. Wang, D. R.: Gray, W. R.
 J.: Inorg. Biochem. 35, 289-303, 1989
 A:Title: Structural and functional diversity of copper-metallothioneins from the American lobster, Homarus americanus (Crustacea: Decapoda)
 A:Accession: A37039; MIM:321575
 A:Status: preliminary
 A:Notes: 1. This is a preliminary report.
 A:Residues: 1-58 <R00>
 C:Superfamily: metallothionein

Query Match 51.0%; Score 26; DB 2; Length 58;
 Best Local Similarity 25.5%; pred. No. 1.1e+02;
 Matches 4; Conservative 0; Alimatches 13; Indels 0; Gaps 0;
 QY 2 CXXXXXXKXKXKXAC 18
 DB 33 CTSCKCKSKDEKATC 49

Search completed: February 13, 2002, 10:11:24
 Job time: 112 sec

